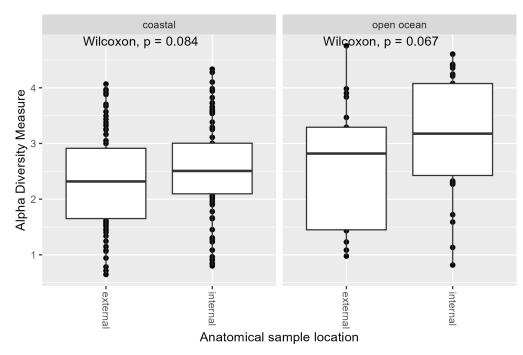
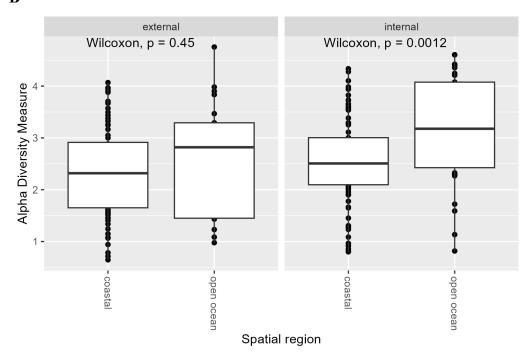
## SUPPLEMENTAL FIGURES/TABLES

A

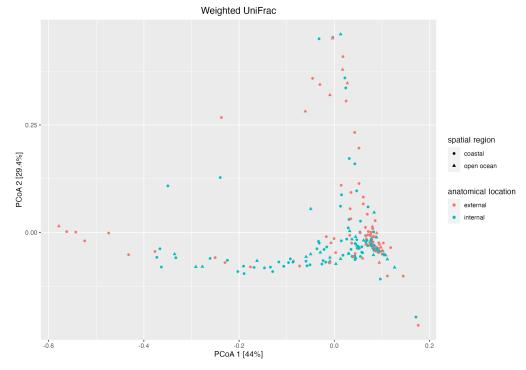


B

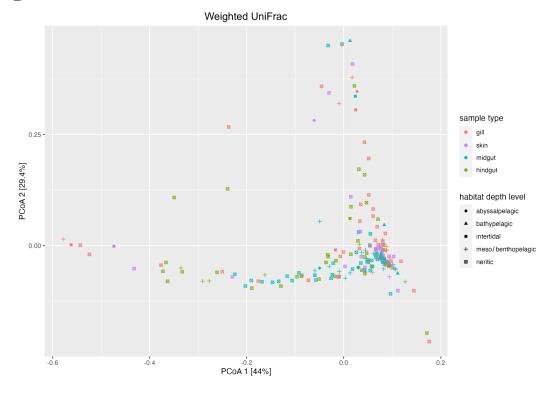


Supplemental Figure 1. Internal sample microbial richness diversity is impacted by spatial region changes. (A) Shannon alpha diversity analysis of anatomical sample location faceted by spatial region shows no significant differences in microbial richness. (B) Shannon alpha diversity analysis of spatial regions faceted by anatomical sample location shows that internal samples have significant differences in microbial richness, but not external. Significant differences between sample categories calculated with Wilcoxson rank sum tests with Bonferroni correction.  $*P < 0.05, P_{adjusted} < 0.013$ .





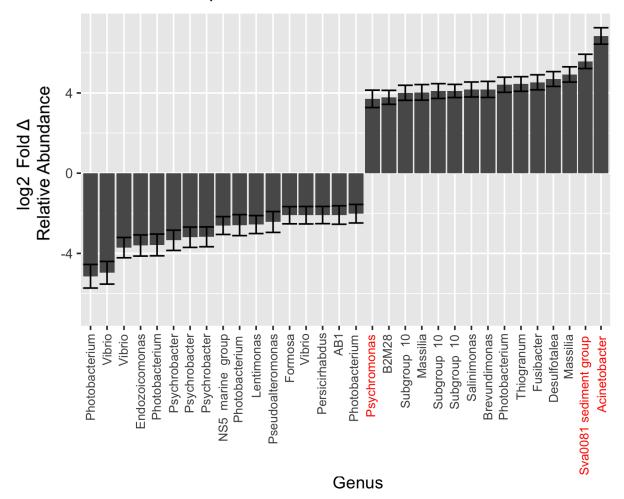
## B



PERMANOVA	df	SS	R2	pseudo-F	p-value
Anatomical location	1	0.1192	0.01235	2.7509	0.030*
Sample type	3	0.3360	0.03481	2.6302	0.007**
Spatial region	1	0.0739	0.00765	1.7049	0.138
Habitat depth level	4	0.2745	0.02843	1.6112	0.095

Supplemental Figure 2. Anatomical region and sample type, but not spatial region or habitat depth, are predictors of beta diversity quantified by weighted UniFrac. (A) and (B) PCoA analysis of variation based on weighted UniFrac distances between microbial communities in all samples. (C) Statistical significance was determined by PERMANOVA. Number of permutations = 999. \*P < 0.05, \*\*P < 0.01.

## Open Ocean Internal vs Coastal Internal



Supplemental Figure 3. Significantly higher abundances of *Psychromonas*, Sva0081 Sediment Group, and *Acinetobacter* in the open ocean internal microbiome compared to coastal internal identified by DESeq2. The y-axis shows the  $\log_2$ -fold change, the x-axis shows the differentially abundant taxa from the open ocean internal microbiomes compared to the coastal internal microbiomes. The same *Psychromonas*, Sva0081 Sediment Group, and *Acinetobacter* seen in the core microbiome analysis are seen increased here, highlighted in red. Significance at P < 0.05.